

## AMENDMENTS

### In the Specification:

Please replace the paragraph beginning at page 5, line 20, with the following rewritten paragraph:

C1 One class of BT-R<sub>1</sub> allelic variants will be proteins that share a high degree of homology with at least a small region of the amino acid sequence provided in Seq. ID No:2, but may further contain a radical departure from the sequence, such as a non-conservative substitution, truncation, insertion or frame shift. Such alleles are termed mutant alleles of BT-R<sub>1</sub> and represent proteins that typically do not perform the same biological functions as does the BT-R<sub>1</sub> variant of Seq. ID No:2.

### In the Claims:

Please replace Claims 1, 4, 5, 8, 13, and 15 with the following replacement claims:

C2 Sub D<sup>1</sup>

1. (Amended) A method to identify agents that bind to a BT-toxin receptor, said method comprising the steps of:

i) contacting an agent with a BT-toxin binding receptor selected from the group consisting of

(a) a cell that has been altered to contain a nucleic acid molecule that encodes a BT toxin receptor having the amino acid sequence of SEQ ID NO:2 and expresses said receptor;

(b) a cell that has been altered to contain a nucleic acid molecule encoding a BT-toxin receptor that hybridizes to the polynucleotide sequence of SEQ ID NO:1 under stringent conditions, wherein said cell expresses said receptor and wherein said receptor has the same sequence as an insect BT toxin receptor that occurs in nature;

(c) a cell that has been altered to contain a nucleic acid molecule encoding a BT-toxin receptor that hybridizes to the polynucleotide sequence of SEQ ID NO:1 under stringent conditions, wherein the cell expresses the receptor and the receptor encoded by the nucleic acid binds to the CryIA(b) toxin;